



IFWO

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/697,912

DATE: 09/16/2004

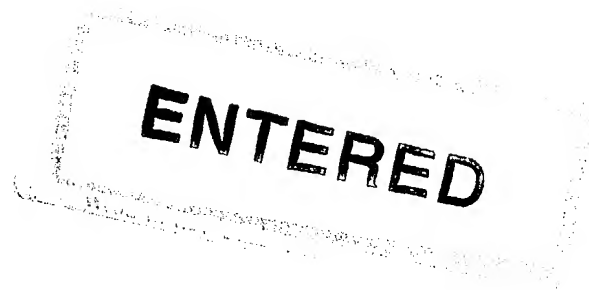
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1 <110> APPLICANT: SADHU, Chanchal et al.
 2 <120> TITLE OF INVENTION: INHIBITORS OF HUMAN PHOSPHATIDYLINOSITOL 3-KINASE DELTA
 3 <130> FILE REFERENCE: 27866/36170C
 4 <140> CURRENT APPLICATION NUMBER: US/10/697,912
 5 <141> CURRENT FILING DATE: 2003-10-30
 6 <150> PRIOR APPLICATION NUMBER: US/10/027,591
 7 <151> PRIOR FILING DATE: 2001-10-19
 8 <150> PRIOR APPLICATION NUMBER: 09/841,341
 9 <151> PRIOR FILING DATE: 2001-04-24
 10 <150> PRIOR APPLICATION NUMBER: 60/199,655
 11 <151> PRIOR FILING DATE: 2000-04-25
 12 <150> PRIOR APPLICATION NUMBER: 60/238,057
 13 <151> PRIOR FILING DATE: 2000-10-25
 14 <160> NUMBER OF SEQ ID NOS: 6
 15 <170> SOFTWARE: PatentIn version 3.0
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 5220
 19 <212> TYPE: DNA
 20 <213> ORGANISM: Human p110delta complete cDNA
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (196)..(3327)
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27	gcggaggggg ctttgctggt ctttcttgga ctattccaga gaggacaact gtcactctggg	180
28	aagtaacaac gcagg atg ccc cct ggg gtg gac tgc ccc atg gaa ttc tgg	231
29	Met Pro Pro Gly Val Asp Cys Pro Met Glu Phe Trp	
30	1 5 10	
31	acc aag gag gag aat cag agc gtt gtg gtt gac ttc ctg ctg ccc aca	279
32	Thr Lys Glu Glu Asn Gln Ser Val Val Val Asp Phe Leu Leu Pro Thr	
33	15 20 25	
34	ggg gtc tac ctg aac ttc cct gtg tcc cgc aat gcc aac ctc agc acc	327
35	Gly Val Tyr Leu Asn Phe Pro Val Ser Arg Asn Ala Asn Leu Ser Thr	
36	30 35 40	
37	atc aag cag ctg ctg tgg cac cgc gcc cag tat gag ccg ctc ttc cac	375
38	Ile Lys Gln Leu Leu Trp His Arg Ala Gln Tyr Glu Pro Leu Phe His	
39	45 50 55 60	
40	atg ctc agt ggc ccc gag gcc tat gtg ttc acc tgc atc aac cag aca	423
41	Met Leu Ser Gly Pro Glu Ala Tyr Val Phe Thr Cys Ile Asn Gln Thr	
42	65 70 75	
43	gcg gag cag caa gag ctg gag gac gag caa cgg cgt ctg tgt gac gtg	471
44	Ala Glu Gln Gln Glu Leu Glu Asp Glu Gln Arg Arg Leu Cys Asp Val	



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47	Gln	Pro	Phe	Leu	Pro	Val	Leu	Arg
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49	gtg	aag	aag	ctc	atc	aac	tca	cag
50	Val	Lys	Lys	Leu	Ile	Asn	Ser	Gln
51		110		115		120		
52	ctc	cac	gag	ttt	gac	tcc	ttg	tgc
53	Leu	His	Glu	Phe	Asp	Ser	Leu	Cys
54		125		130		135		140
55	gcc	aag	atg	tgc	caa	ttc	tgc	gag
56	Ala	Lys	Met	Cys	Gln	Phe	Cys	Glu
57			145			150		155
58	ctg	ggc	tgg	gag	gcc	tgg	ctg	cag
59	Leu	Gly	Trp	Glu	Ala	Trp	Leu	Gln
60			160			165		170
61	ccc	tcg	gct	caa	acc	tgg	ggg	cct
62	Pro	Ser	Ala	Gln	Thr	Trp	Gly	Pro
63			175			180		185
64	gcc	ctt	ctg	gtc	aac	gtt	aag	ttt
65	Ala	Leu	Leu	Val	Asn	Val	Lys	Phe
66		190				195		200
67	ttc	cag	gtg	tcc	acc	aag	gac	gtg
68	Phe	Gln	Val	Ser	Thr	Lys	Asp	Val
69		205				210		215
70	ctg	cgg	aag	aag	gcc	aca	gtg	ttc
71	Leu	Arg	Lys	Lys	Ala	Thr	Val	Phe
72				225				230
73	gaa	gac	tac	acg	ctg	cag	gtg	aac
74	Glu	Asp	Tyr	Thr	Leu	Gln	Val	Asn
75			240				245	250
76	aac	tac	ccg	ctc	tgc	cag	ttc	cag
77	Asn	Tyr	Pro	Leu	Cys	Gln	Phe	Gln
78			255				260	265
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80	Gly	Leu	Thr	Pro	His	Leu	Thr	Met
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82	atg	cgg	gat	gag	cag	agc	aac	cct
83	Met	Arg	Asp	Glu	Gln	Ser	Asn	Pro
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85	gcc	aaa	cca	cct	ccc	att	cct	gcg
86	Ala	Lys	Pro	Pro	Pro	Ile	Pro	Ala
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88	tgg	tcc	ctg	gag	cag	ccg	ttc	cgc
89	Trp	Ser	Leu	Glu	Gln	Pro	Phe	Arg
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91	gtg	aac	gcc	gac	gag	cgg	atg	aag
92	Val	Asn	Ala	Asp	Glu	Arg	Met	Lys
93			335					340

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95	His Gly Asn Glu Met Leu Cys Lys Thr Val Ser Ser Ser Glu Val Ser	
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97	gtg tgc tcg gag ccc gtg tgg aag cag cgg ctg gag ttc gac atc aac	1335
98	Val Cys Ser Glu Pro Val Trp Lys Gln Arg Leu Glu Phe Asp Ile Asn	
99	365 370 375 380	
100	atc tgc gac ctg ccc cgc atg gcc cgt ctc tgc ttt gcg ctg tac gcc	1383
101	Ile Cys Asp Leu Pro Arg Met Ala Arg Leu Cys Phe Ala Leu Tyr Ala	
102	385 390 395	
103	gtg atc gag aaa gcc aag aag gct cgc tcc acc aag aag aag tcc aag	1431
104	Val Ile Glu Lys Ala Lys Lys Ala Arg Ser Thr Lys Lys Lys Ser Lys	
105	400 405 410	
106	aag gcg gac tgc ccc att gcc tgg gcc aac ctc atg ctg ttt gac tac	1479
107	Lys Ala Asp Cys Pro Ile Ala Trp Ala Asn Leu Met Leu Phe Asp Tyr	
108	415 420 425	
109	aag gac cag ctt aag acc ggg gaa cgc tgc ctc tac atg tgg ccc tcc	1527
110	Lys Asp Gln Leu Lys Thr Gly Glu Arg Cys Leu Tyr Met Trp Pro Ser	
111	430 435 440	
112	gtc cca gat gag aag ggc gag ctg ctg aac ccc acg ggc act gtg cgc	1575
113	Val Pro Asp Glu Lys Gly Glu Leu Leu Asn Pro Thr Gly Thr Val Arg	
114	445 450 455 460	
115	agt aac ccc aac acg gat agc gcc gct gcc ctg ctc atc tgc ctg ccc	1623
116	Ser Asn Pro Asn Thr Asp Ser Ala Ala Leu Leu Ile Cys Leu Pro	
117	465 470 475	
118	gag gtg gcc ccg cac ccc gtg tac tac ccc gcc ctg gag aag atc ttg	1671
119	Glu Val Ala Pro His Pro Val Tyr Tyr Pro Ala Leu Glu Lys Ile Leu	
120	480 485 490	
121	gag ctg ggg cga cac agc gag tgt gtg cat gtc acc gag gag gag cag	1719
122	Glu Leu Gly Arg His Ser Glu Cys Val His Val Thr Glu Glu Glu Gln	
123	495 500 505	
124	ctg cag ctg cgg gaa atc ctg gag cgg cgg ggg tct ggg gag ctg tat	1767
125	Leu Gln Leu Arg Glu Ile Leu Glu Arg Arg Gly Ser Gly Glu Leu Tyr	
126	510 515 520	
127	gag cac gag aag gac ctg gtg tgg aag ctg cgg cat gaa gtc cag gag	1815
128	Glu His Glu Lys Asp Leu Val Trp Lys Leu Arg His Glu Val Gln Glu	
129	525 530 535 540	
130	cac ttc ccg gag gcg cta gcc cgg ctg ctg ctg gtc acc aag tgg aac	1863
131	His Phe Pro Glu Ala Leu Ala Arg Leu Leu Leu Val Thr Lys Trp Asn	
132	545 550 555	
133	aag cat gag gat gtg gcc cag atg ctc tac ctg ctg tgc tcc tgg ccg	1911
134	Lys His Glu Asp Val Ala Gln Met Leu Tyr Leu Leu Cys Ser Trp Pro	
135	560 565 570	
136	gag ctg ccc gtc ctg agc gcc ctg gag ctg cta gac ttc agc ttc ccc	1959
137	Glu Leu Pro Val Leu Ser Ala Leu Glu Leu Leu Asp Phe Ser Phe Pro	
138	575 580 585	
139	gat tgc cac gta ggc tcc ttc gcc atc aag tcg ctg cgg aaa ctg acg	2007
140	Asp Cys His Val Gly Ser Phe Ala Ile Lys Ser Leu Arg Lys Leu Thr	
141	590 595 600	
142	gac gat gag ctg ttc cag tac ctg ctg cag ctg gtg cag gtg ctc aag	2055

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143	Asp	Asp	Glu	Leu	Phe	Gln	Tyr	Leu	Leu	Gln	Leu	Val	Gln	Val	Leu	Lys	
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145	tac	gag	tcc	tac	ctg	gac	tgc	gag	ctg	acc	aaa	ttc	ctg	ctg	gac	cgg	2103
146	Tyr	Glu	Ser	Tyr	Leu	Asp	Cys	Glu	Leu	Thr	Lys	Phe	Leu	Leu	Asp	Arg	
147					625					630						635	
148	gcc	ctg	gcc	aac	cgc	aag	atc	ggc	cac	ttc	ctt	ttc	tgg	cac	ctc	cgc	2151
149	Ala	Leu	Ala	Asn	Arg	Lys	Ile	Gly	His	Phe	Leu	Phe	Trp	His	Leu	Arg	
150				640					645						650		
151	tcc	gag	atg	cac	gtg	ccg	tgc	gtg	gcc	ctg	cgc	ttc	ggc	ctc	atc	ctg	2199
152	Ser	Glu	Met	His	Val	Pro	Ser	Val	Ala	Leu	Arg	Phe	Gly	Leu	Ile	Leu	
153			655					660					665				
154	gag	gcc	tac	tgc	agg	ggc	agc	acc	cac	cac	atg	aag	gtg	ctg	atg	aag	2247
155	Glu	Ala	Tyr	Cys	Arg	Gly	Ser	Thr	His	His	Met	Lys	Val	Leu	Met	Lys	
156		670				675						680					
157	cag	ggg	gaa	gca	ctg	agc	aaa	ctg	aag	gcc	ctg	aat	gac	ttc	gtc	aag	2295
158	Gln	Gly	Glu	Ala	Leu	Ser	Lys	Leu	Lys	Ala	Leu	Asn	Asp	Phe	Val	Lys	
159	685					690					695					700	
160	ctg	agc	tct	cag	aag	acc	ccc	aag	ccc	cag	acc	aag	gag	ctg	atg	cac	2343
161	Leu	Ser	Ser	Gln	Lys	Thr	Pro	Lys	Pro	Gln	Thr	Lys	Glu	Leu	Met	His	
162				705						710					715		
163	ttg	tgc	atg	cgg	cag	gag	gcc	tac	cta	gag	gcc	ctc	tcc	cac	ctg	cag	2391
164	Leu	Cys	Met	Arg	Gln	Glu	Ala	Tyr	Leu	Glu	Ala	Leu	Ser	His	Leu	Gln	
165			720					725						730			
166	tcc	cca	ctc	gac	ccc	agc	acc	ctg	ctg	gct	gaa	gtc	tgc	gtg	gag	cag	2439
167	Ser	Pro	Leu	Asp	Pro	Ser	Thr	Leu	Leu	Ala	Glu	Val	Cys	Val	Glu	Gln	
168			735					740					745				
169	tgc	acc	ttc	atg	gac	tcc	aag	atg	aag	ccc	ctg	tgg	atc	atg	tac	agc	2487
170	Cys	Thr	Phe	Met	Asp	Ser	Lys	Met	Lys	Pro	Leu	Trp	Ile	Met	Tyr	Ser	
171		750				755						760					
172	aac	gag	gag	gca	ggc	agc	ggc	ggc	agc	gtg	ggc	atc	atc	ttt	aag	aac	2535
173	Asn	Glu	Glu	Ala	Gly	Ser	Gly	Gly	Ser	Val	Gly	Ile	Ile	Phe	Lys	Asn	
174	765				770					775						780	
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176	Gly	Asp	Asp	Leu	Arg	Gln	Asp	Met	Leu	Thr	Leu	Gln	Met	Ile	Gln	Leu	
177				785					790					795			
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182	Tyr	Gly	Cys	Leu	Pro	Thr	Gly	Asp	Arg	Thr	Gly	Leu	Ile	Glu	Val	Val	
183			815					820					825				
184	ctc	cgt	tca	gac	acc	atc	gcc	aac	atc	caa	ctc	aac	aag	agc	aac	atg	2727
185	Leu	Arg	Ser	Asp	Thr	Ile	Ala	Asn	Ile	Gln	Leu	Asn	Lys	Ser	Asn	Met	
186		830				835						840					
187	gca	gcc	aca	gcc	gcc	ttc	aac	aag	gat	gcc	ctg	ctc	aac	tgg	ctg	aag	2775
188	Ala	Ala	Thr	Ala	Ala	Phe	Asn	Lys	Asp	Ala	Leu	Leu	Asn	Trp	Leu	Lys	
189	845					850					855					860	
190	tcc	aag	aac	ccg	ggg	gag	gcc	ctg	gat	cga	gcc	att	gag	gag	ttc	acc	2823
191	Ser	Lys	Asn	Pro	Gly	Glu	Ala	Leu	Asp	Arg	Ala	Ile	Glu	Glu	Phe	Thr	

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195		880		885		890		
196	gat cgg cac agc gac aac atc atg atc cga gag agt ggg cag ctg ttc							2919
197	Asp Arg His Ser Asp Asn Ile Met Ile Arg Glu Ser Gly Gln Leu Phe							
198		895		900		905		
199	cac att gat ttt ggc cac ttt ctg ggg aat ttc aag acc aag ttt gga							2967
200	His Ile Asp Phe Gly His Phe Leu Gly Asn Phe Lys Thr Lys Phe Gly							
201		910		915		920		
202	atc aac cgc gag cgt gtc cca ttc atc ctc acc tat gac ttt gtc cat							3015
203	Ile Asn Arg Glu Arg Val Pro Phe Ile Leu Thr Tyr Asp Phe Val His							
204		925		930		935		940
205	gtg att cag cag ggg aag act aat aat agt gag aaa ttt gaa cgg ttc							3063
206	Val Ile Gln Gln Gly Lys Thr Asn Asn Ser Glu Lys Phe Glu Arg Phe							
207		945		950		955		
208	cgg ggc tac tgt gaa agg gcc tac acc atc ctg cgg cgc cac ggg ctt							3111
209	Arg Gly Tyr Cys Glu Arg Ala Tyr Thr Ile Leu Arg Arg His Gly Leu							
210		960		965		970		
211	ctc ttc ctc cac ctc ttt gcc ctg atg cgg gcg gca ggc ctg cct gag							3159
212	Leu Phe Leu His Leu Phe Ala Leu Met Arg Ala Ala Gly Leu Pro Glu							
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217	ggg aaa aca gag gag gag gca ctg aag cac ttc cga gtg aag ttt							3252
218	Gly Lys Thr Glu Glu Glu Ala Leu Lys His Phe Arg Val Lys Phe							
219		1005		1010		1015		
220	aac gaa gcc ctc cgt gag agc tgg aaa acc aaa gtg aac tgg ctg							3297
221	Asn Glu Ala Leu Arg Glu Ser Trp Lys Thr Lys Val Asn Trp Leu							
222		1020		1025		1030		
223	gcc cac aac gtg tcc aaa gac aac agg cag tagtggtcc tcccagcct							3347
224	Ala His Asn Val Ser Lys Asp Asn Arg Gln							
225		1035		1040				
226	gggcccaaga ggaggcggct gcgggtcgtg gggaccaagc acattggtcc taaaggggct							3407
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228	gttattttatt tatgacttga aatagtttaa ggagctaaac agccataaac ggaaacgcct							3527
229	ccttcattca gcggcggtgc tgggcccccc gaggtgcac ctggctctcg gctgaggatt							3587
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